

#5

1/47

+

09854355 020402

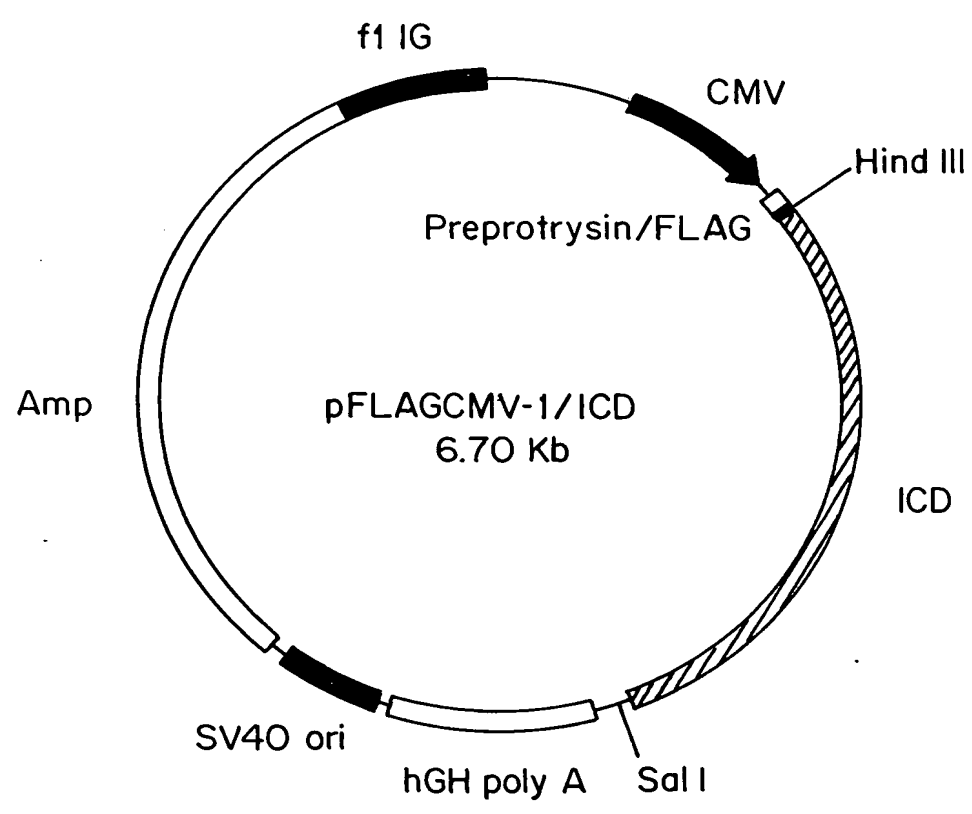
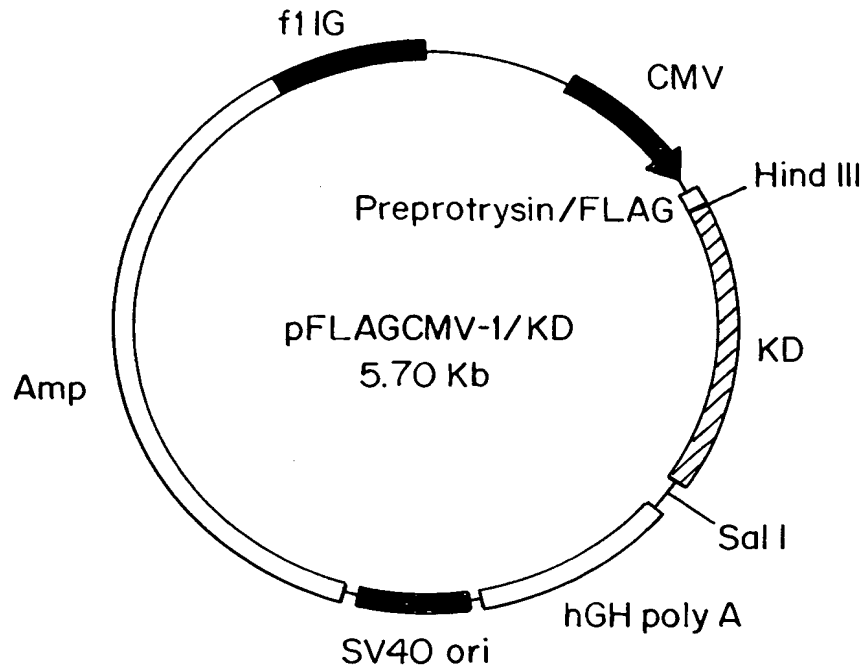
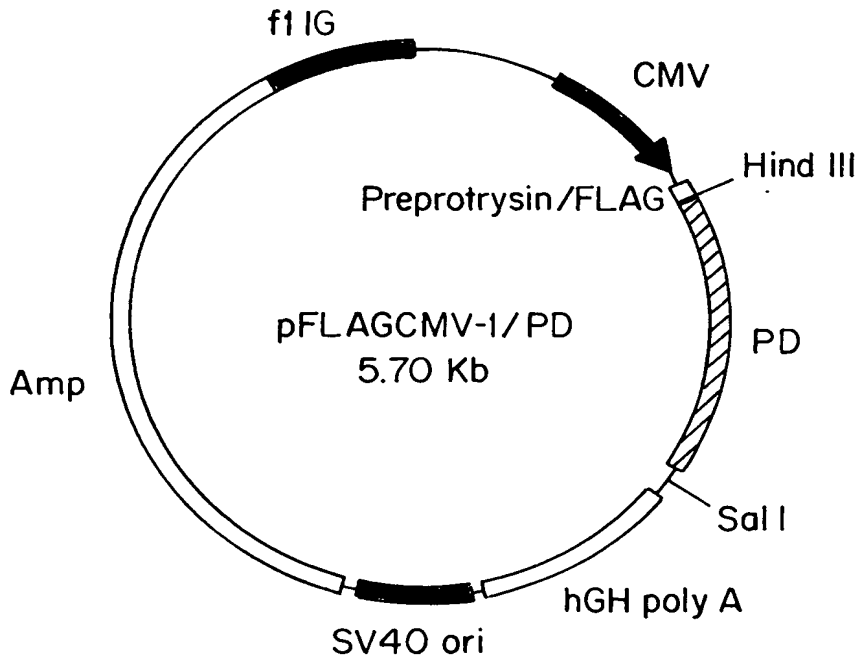


FIG. 1.

+

**FIG. 2.****FIG. 3.**

+

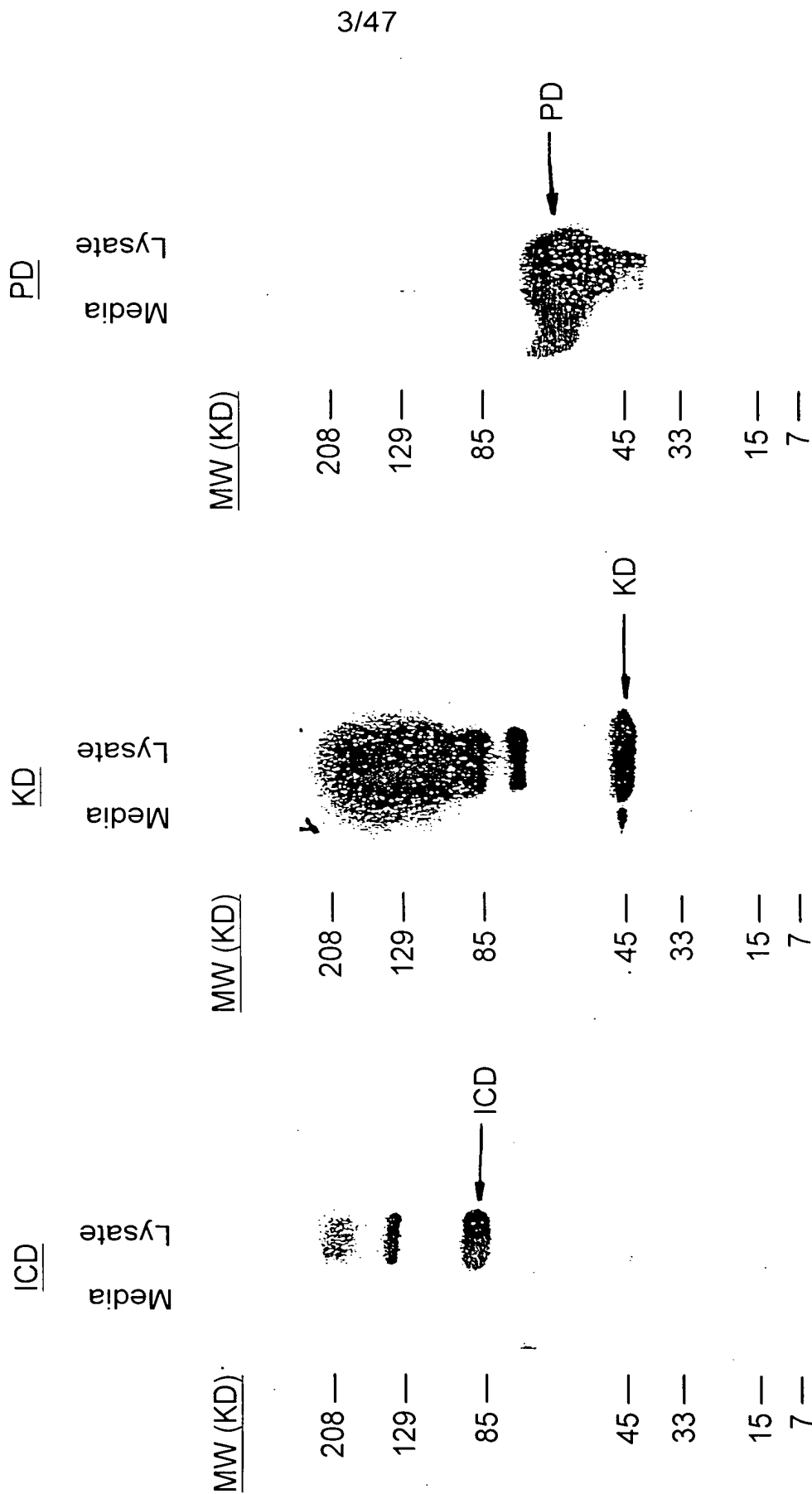
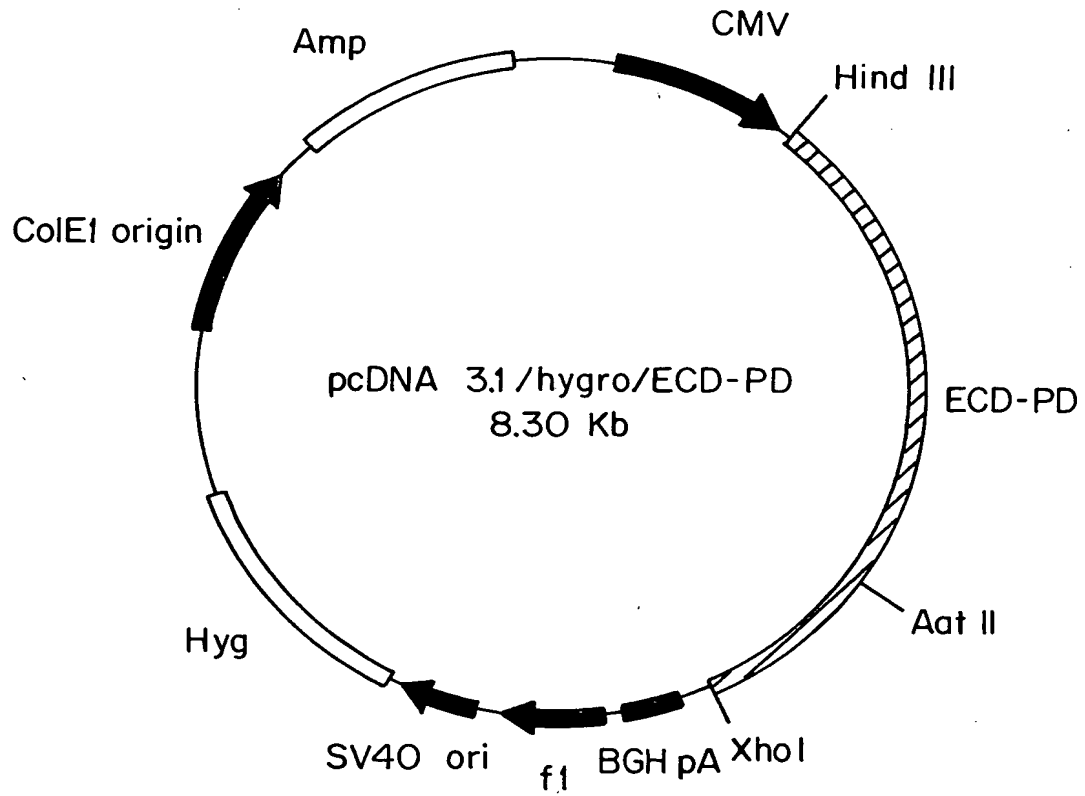


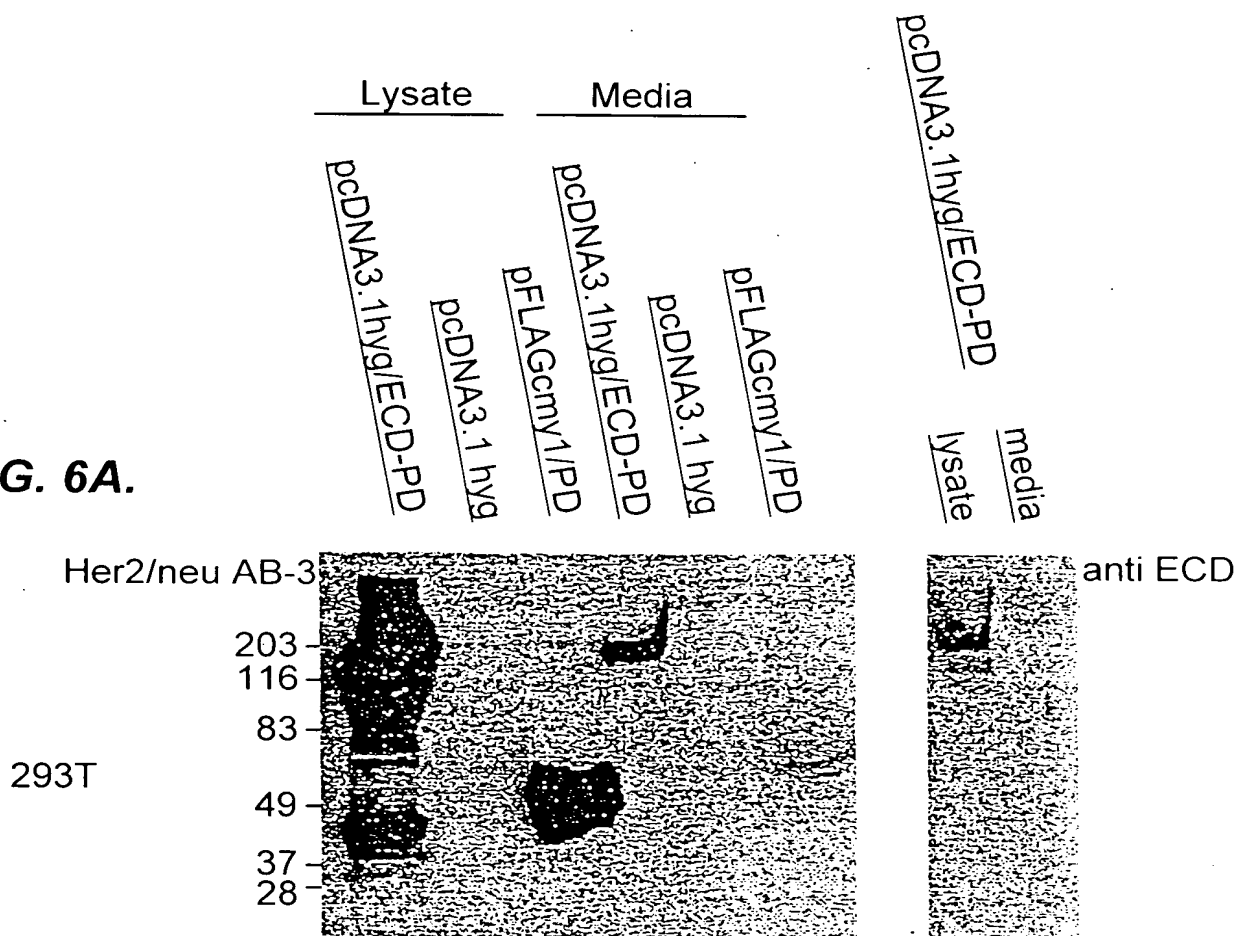
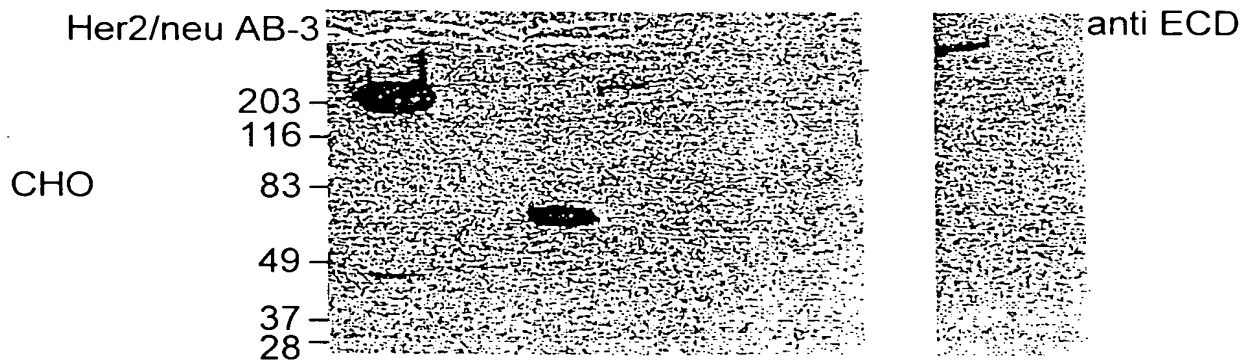
FIG. 4.

+

**FIG. 5.**



pcDNA3.1hyg/ECD-PD expression

FIG. 6A.**FIG. 6B.**

09854356-020402



09854356-020402

+

6/47

Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu	
1				5					10					15		
Pro	Pro	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys	
			20					25					30			
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His	
		35					40					45				
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr	
	50					55					60					
Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val	
65					70					75					80	
Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu	
				85					90					95		
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr	
			100					105					110			
Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro	
		115					120					125				
Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser	
	130					135					140					
Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	
145					150					155					160	
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	
				165					170					175		
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	
			180					185					190			
His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	
		195					200					205				
Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys	
	210					215					220					
Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	
225					230					235					240	
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	
				245					250					255		

FIG. 7. (SEQ ID NO: 1)

+

0934356-020400

+

7/47

His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val
			260					265					270		
Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg
		275					280					285			
Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu
	290					295					300				
Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln
305					310					315					320
Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys
				325					330					335	
Pro	Cys	Ala	Arg	Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu
			340					345					350		
Val	Arg	Ala	Val	Thr	Ser	Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys
		355					360					365			
Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp
	370					375					380				
Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe
385					390					395					400
Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro
				405					410					415	
Asp	Ser	Leu	Pro	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg
			420					425					430		
Gly	Arg	Ile	Leu	His	Asn	Gly	Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu
		435					440					445			
Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	Leu	Gly	Ser	Gly
	450					455					460				
Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val
465					470					475					480
Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr
				485					490					495	
Ala	Asn	Arg	Pro	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His
			500					505					510		

FIG. 7. (CONTINUED)

+

+

D

+

09854356-020402

+

9/47

Asp	Glu	Ala	Tyr	Val	Met	Ala	Gly	Val	Gly	Ser	Pro	Tyr	Val	Ser	Arg
770						775					780				
Leu	Leu	Gly	Ile	Cys	Leu	Thr	Ser	Thr	Val	Gln	Leu	Val	Thr	Gln	Leu
785					790					795					800
Met	Pro	Tyr	Gly	Cys	Leu	Leu	Asp	His	Val	Arg	Glu	Asn	Arg	Gly	Arg
				805					810					815	
Leu	Gly	Ser	Gln	Asp	Leu	Leu	Asn	Trp	Cys	Met	Gln	Ile	Ala	Lys	Gly
			820					825					830		
Met	Ser	Tyr	Leu	Glu	Asp	Val	Arg	Leu	Val	His	Arg	Asp	Leu	Ala	Ala
		835					840					845			
Arg	Asn	Val	Leu	Val	Lys	Ser	Pro	Asn	His	Val	Lys	Ile	Thr	Asp	Phe
	850					855					860				
Gly	Leu	Ala	Arg	Leu	Leu	Asp	Ile	Asp	Glu	Thr	Glu	Tyr	His	Ala	Asp
865					870					875					880
Gly	Gly	Lys	Val	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Ser	Ile	Leu	Arg
				885					890					895	
Arg	Arg	Phe	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Val
			900					905					910		
Trp	Glu	Leu	Met	Thr	Phe	Gly	Ala	Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Ala
		915					920					925			
Arg	Glu	Ile	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu	Arg	Leu	Pro	Gln	Pro
	930					935					940				
Pro	Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Ile	Met	Val	Lys	Cys	Trp	Met
945					950					955					960
Ile	Asp	Ser	Glu	Cys	Arg	Pro	Arg	Phe	Arg	Glu	Leu	Val	Ser	Glu	Phe
				965					970					975	
Ser	Arg	Met	Ala	Arg	Asp	Pro	Gln	Arg	Phe	Val	Val	Ile	Gln	Asn	Glu
			980					985					990		
Asp	Leu	Gly	Pro	Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr	Arg	Ser	Leu
		995				1000						1005			
Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	Glu	Glu	Tyr	Leu
1010						1015					1020				

FIG. 7. (CONTINUED)

+

+

10/47

Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly
 1025 1030 1035 1040
 Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly
 1045 1050 1055
 Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg
 1060 1065 1070
 Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly
 1075 1080 1085
 Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His
 1090 1095 1100
 Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu
 1105 1110 1115 1120
 Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln
 1125 1130 1135
 Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro
 1140 1145 1150
 Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
 1155 1160 1165
 Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val
 1170 1175 1180
 Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
 1185 1190 1195 1200
 Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala
 1205 1210 1215
 Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala
 1220 1225 1230
 Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
 1235 1240 1245
 Leu Gly Leu Asp Val Pro Val * *
 1250 1255 1257

FIG. 7. (CONTINUED)

+

0084356 020400

+

11/47

Met	Glu	Leu	Ala	Ala	Trp	Cys	Arg	Trp	Gly	Phe	Leu	Leu	Ala	Leu	Leu			
1				5					10					15				
Pro	Pro	Gly	Ile	Ala	Gly	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys			
			20					25					30					
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His			
			35				40					45						
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr			
	50					55					60							
Val	Pro	Ala	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val			
65					70					75					80			
Gln	Gly	Tyr	Met	Leu	Ile	Ala	His	Asn	Gln	Val	Lys	Arg	Val	Pro	Leu			
				85					90					95				
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Lys	Tyr			
			100					105					110					
Ala	Leu	Ala	Val	Leu	Asp	Asn	Arg	Asp	Pro	Gln	Asp	Asn	Val	Ala	Ala			
		115					120					125						
Ser	Thr	Pro	Gly	Arg	Thr	Pro	Glu	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg			
			130			135					140							
Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Arg	Gly	Asn	Pro			
145					150					155					160			
Gln	Leu	Cys	Tyr	Gln	Asp	Met	Val	Leu	Trp	Lys	Asp	Val	Phe	Arg	Lys			
				165					170					175				
Asn	Asn	Gln	Leu	Ala	Pro	Val	Asp	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala			
			180					185					190					
Cys	Pro	Pro	Cys	Ala	Pro	Ala	Cys	Lys	Asp	Asn	His	Cys	Trp	Gly	Glu			
		195					200					205						
Ser	Pro	Glu	Asp	Cys	Gln	Ile	Leu	Thr	Gly	Thr	Ile	Cys	Thr	Ser	Gly			
		210				215					220							
Cys	Ala	Arg	Cys	Lys	Gly	Arg	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln			
225					230					235					240			
Cys	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys			
			245						250					255				

FIG. 8. (SEQ ID NO:2)

+

204020" 9545860

+

060402

+

+

13/47

Asn	Ser	Leu	Cys	Ala	His	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln				
		515					520					525							
Cys	Val	Asn	Cys	Ser	His	Phe	Leu	Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu				
	530					535					540								
Cys	Arg	Val	Trp	Lys	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Ser	Asp	Lys	Arg				
545					550					555					560				
Cys	Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Ser	Ser	Glu	Thr				
				565					570					575					
Cys	Phe	Gly	Ser	Glu	Ala	Asp	Gln	Cys	Ala	Ala	Cys	Ala	His	Tyr	Lys				
			580					585					590						
Asp	Ser	Ser	Ser	Cys	Val	Ala	Arg	Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp				
		595					600					605							
Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	Tyr	Pro	Asp	Glu	Glu	Gly	Ile	Cys				
	610					615					620								
Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Glu				
625					630					635					640				
Arg	Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Val	Thr	Phe	Ile	Ile				
				645					650					655					
Ala	Thr	Val	Glu	Gly	Val	Leu	Leu	Phe	Leu	Ile	Leu	Val	Val	Val	Val				
			660					665					670						
Gly	Ile	Leu	Ile	Lys	Arg	Arg	Arg	Gln	Lys	Ile	Arg	Lys	Tyr	Thr	Met				
	675					680						685							
Arg	Arg	Leu	Leu	Gln	Glu	Thr	Glu	Leu	Val	Glu	Pro	Leu	Thr	Pro	Ser				
	690					695					700								
Gly	Ala	Met	Pro	Asn	Gln	Ala	Gln	Met	Arg	Ile	Leu	Lys	Glu	Thr	Glu				
705					710					715					720				
Leu	Arg	Lys	Val	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr				
				725					730					735					
Lys	Gly	Ile	Trp	Ile	Pro	Asp	Gly	Glu	Asn	Val	Lys	Ile	Pro	Val	Ala				
			740					745					750						
Ile	Lys	Val	Leu	Arg	Glu	Asn	Thr	Ser	Pro	Lys	Ala	Asn	Lys	Glu	Ile				
	755					760						765							

FIG. 8. (CONTINUED)

+

09854356-020402

+

[illegible]

+

+

15/47

Leu Val Pro Gln Gln Gly Phe Phe Ser Pro Asp Pro Thr Pro Gly Thr
 1025 1030 1035 1040
 Gly Ser Thr Ala His Arg Arg His Arg Ser Ser Ser Thr Arg Ser Gly
 1045 1050 1055
 Gly Gly Glu Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Gly Pro Pro
 1060 1065 1070
 Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp
 1075 1080 1085
 Gly Asp Leu Ala Met Gly Val Thr Lys Gly Leu Gln Ser Leu Ser Pro
 1090 1095 1100
 His Asp Leu Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Leu Pro
 1105 1110 1115 1120
 Leu Pro Pro Glu Thr Asp Gly Tyr Val Ala Pro Leu Ala Cys Ser Pro
 1125 1130 1135
 Gln Pro Glu Tyr Val Asn Gln Ser Glu Val Gln Pro Gln Pro Pro Leu
 1140 1145 1150
 Thr Pro Glu Gly Pro Leu Pro Pro Val Arg Pro Ala Gly Ala Thr Leu
 1155 1160 1165
 Glu Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp
 1170 1175 1180
 Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Val Pro
 1185 1190 1195 1200
 Arg Glu Gly Thr Ala Ser Pro Pro His Pro Ser Pro Ala Phe Ser Pro
 1205 1210 1215
 Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asn Ser Ser Glu Gln Gly
 1220 1225 1230
 Pro Pro Pro Ser Asn Phe Glu Gly Thr Pro Thr Ala Glu Asn Pro Glu
 1235 1240 1245
 Tyr Leu Gly Leu Asp Val Pro Val * *
 1250 1255 1258

FIG. 8. (CONTINUED)

+

204020" 9546860

09054356 020402

+

16/47

Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu	
1				5					10					15		
Pro	Pro	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys	
			20					25					30			
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His	
		35					40					45				
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr	
	50					55					60					
Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val	
65					70					75					80	
Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu	
				85					90					95		
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr	
			100					105					110			
Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro	
		115					120					125				
Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser	
	130					135					140					
Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	
145					150					155					160	
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	
				165					170					175		
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	
			180					185					190			
His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	
		195					200					205				
Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys	
	210					215					220					
Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	
225					230					235					240	
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	
				245					250					255		

FIG. 9. (SEQ ID NO: 3)

+

+

17/47

His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val
			260					265					270		
Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg
		275					280					285			
Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu
	290					295					300				
Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln
305					310					315					320
Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys
				325					330					335	
Pro	Cys	Ala	Arg	Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu
			340					345					350		
Val	Arg	Ala	Val	Thr	Ser	Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys
		355					360					365			
Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp
	370					375					380				
Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe
385					390					395					400
Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro
			405					410						415	
Asp	Ser	Leu	Pro	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg
			420					425					430		
Gly	Arg	Ile	Leu	His	Asn	Gly	Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu
		435					440					445			
Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	Leu	Gly	Ser	Gly
	450					455					460				
Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val
465					470					475					480
Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr
				485				490						495	
Ala	Asn	Arg	Pro	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His
			500					505					510		

FIG. 9. (CONTINUED)

+

0935456-02040

+

18/47

Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys
		515					520					525			
Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu	Cys
		530				535					540				
Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys
545					550					555					560
Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys
				565					570					575	
Phe	Gly	Pro	Glu	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp
			580					585					590		
Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu
		595					600					605			
Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	Gly	Ala	Cys	Gln
	610					615					620				
Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys
625				630						635					640
Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser			
				645					650			653			

FIG. 9. (CONTINUED)

Gln	Asn	Glu	Asp	Leu	Gly	Pro	Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr
1				5					10					15	
Arg	Ser	Leu	Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	Glu
			20					25					30		
Glu	Tyr	Leu	Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro
		35					40					45			
Gly	Ala	Gly	Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	Ser	Thr	Arg
	50					55					60				
Ser	Gly	Gly	Gly	Asp	Leu	Thr	Leu	Gly	Leu	Glu	Pro	Ser	Glu	Glu	Glu
65					70					75					80
Ala	Pro	Arg	Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	Ala	Gly	Ser	Asp	Val
				85					90					95	

FIG. 10. (SEQ ID NO: 4)

+

0954356-020400

09354356-020402

+

19/47

Phe	Asp	Gly	Asp	Leu	Gly	Met	Gly	Ala	Ala	Lys	Gly	Leu	Gln	Ser	Leu	
			100					105					110			
Pro	Thr	His	Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp	Pro	Thr	
		115					120					125				
Val	Pro	Leu	Pro	Ser	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu	Thr	Cys	
		130				135					140					
Ser	Pro	Gln	Pro	Glu	Tyr	Val	Asn	Gln	Pro	Asp	Val	Arg	Pro	Gln	Pro	
145					150					155					160	
Pro	Ser	Pro	Arg	Glu	Gly	Pro	Leu	Pro	Ala	Ala	Arg	Pro	Ala	Gly	Ala	
				165					170					175		
Thr	Leu	Glu	Arg	Pro	Lys	Thr	Leu	Ser	Pro	Gly	Lys	Asn	Gly	Val	Val	
			180					185					190			
Lys	Asp	Val	Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu	Tyr	Leu	
		195					200					205				
Thr	Pro	Gln	Gly	Gly	Ala	Ala	Pro	Gln	Pro	His	Pro	Pro	Pro	Ala	Phe	
		210				215					220					
Ser	Pro	Ala	Phe	Asp	Asn	Leu	Tyr	Tyr	Trp	Asp	Gln	Asp	Pro	Pro	Glu	
225					230					235					240	
Arg	Gly	Ala	Pro	Pro	Ser	Thr	Phe	Lys	Gly	Thr	Pro	Thr	Ala	Glu	Asn	
				245					250					255		
Pro	Glu	Tyr	Leu	Gly	Leu	Asp	Val	Pro	Val	*						
			260					265		267						

FIG. 10. (CONTINUED)

Gln	Asn	Glu	Asp	Leu	Gly	Pro	Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr	
1				5					10					15		
Arg	Ser	Leu	Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	Glu	
			20					25					30			
Glu	Tyr	Leu	Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro	
		35					40					45				
Gly	Ala	Gly	Gly	Met	Val	His	His	Arg	His	Arg	*					
	50					55					60					

FIG. 11. (SEQ ID NO: 5)

+

+

20/47

Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu	
1				5					10					15		
Pro	Pro	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys	
			20					25					30			
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His	
		35					40					45				
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr	
	50					55					60					
Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val	
65					70					75					80	
Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu	
				85					90					95		
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr	
			100					105					110			
Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro	
		115					120					125				
Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser	
	130					135					140					
Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	
145					150					155					160	
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	
				165					170					175		
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	
			180					185					190			
His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	
		195					200					205				
Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys	
	210					215					220					
Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	
225					230					235					240	
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	
				245					250					255		

FIG. 12. (SEQ ID NO: 6)

+

09854356 020402

+

[illegible]

+

+

22/47

Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys
		515					520					525			
Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu	Cys
	530					535					540				
Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys
545					550					555					560
Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys
				565					570					575	
Phe	Gly	Pro	Glu	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp
			580					585					590		
Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu
		595					600					605			
Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	Gly	Ala	Cys	Gln
	610					615					620				
Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys
625					630					635					640
Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser	Gln	Asn	Glu
				645					650					655	
Asp	Leu	Gly	Pro	Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr	Arg	Ser	Leu
			660					665					670		
Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	Glu	Glu	Tyr	Leu
		675					680					685			
Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro	Gly	Ala	Gly
	690					695					700				
Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	Ser	Thr	Arg	Ser	Gly	Gly
705					710					715					720
Gly	Asp	Leu	Thr	Leu	Gly	Leu	Glu	Pro	Ser	Glu	Glu	Glu	Ala	Pro	Arg
				725					730					735	
Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	Ala	Gly	Ser	Asp	Val	Phe	Asp	Gly
			740					745					750		
Asp	Leu	Gly	Met	Gly	Ala	Ala	Lys	Gly	Leu	Gln	Ser	Leu	Pro	Thr	His
		755					760					765			

FIG. 12. (CONTINUED)

+

09854356-020402

+

23/47

Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp	Pro	Thr	Val	Pro	Leu
770						775					780				
Pro	Ser	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu	Thr	Cys	Ser	Pro	Gln
785					790					795					800
Pro	Glu	Tyr	Val	Asn	Gln	Pro	Asp	Val	Arg	Pro	Gln	Pro	Pro	Ser	Pro
				805					810					815	
Arg	Glu	Gly	Pro	Leu	Pro	Ala	Ala	Arg	Pro	Ala	Gly	Ala	Thr	Leu	Glu
			820					825					830		
Arg	Pro	Lys	Thr	Leu	Ser	Pro	Gly	Lys	Asn	Gly	Val	Val	Lys	Asp	Val
		835					840					845			
Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu	Tyr	Leu	Thr	Pro	Gln
	850					855					860				
Gly	Gly	Ala	Ala	Pro	Gln	Pro	His	Pro	Pro	Pro	Ala	Phe	Ser	Pro	Ala
865					870					875					880
Phe	Asp	Asn	Leu	Tyr	Tyr	Trp	Asp	Gln	Asp	Pro	Pro	Glu	Arg	Gly	Ala
				885					890					895	
Pro	Pro	Ser	Thr	Phe	Lys	Gly	Thr	Pro	Thr	Ala	Glu	Asn	Pro	Glu	Tyr
			900					905					910		
Leu	Gly	Leu	Asp	Val	Pro	Val	*								
	915					920									

FIG. 12. (CONTINUED)

09854356-020403

+

+

24/47

Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu	1	5	10	15
Pro	Pro	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys	20	25	30	
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His	35	40	45	
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr	50	55	60	
Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val	65	70	75	80
Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu	85	90	95	
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr	100	105	110	
Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro	115	120	125	
Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser	130	135	140	
Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	145	150	155	160
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	165	170	175	
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	180	185	190	
His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	195	200	205	
Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys	210	215	220	
Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	225	230	235	240
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	245	250	255	

FIG. 13. (SEQ ID NO: 7)

+

204020"954356"02040

+

25/47

His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val
			260					265					270		
Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg
		275					280					285			
Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu
	290					295					300				
Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln
305					310					315					320
Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys
				325					330					335	
Pro	Cys	Ala	Arg	Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu
			340					345					350		
Val	Arg	Ala	Val	Thr	Ser	Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys
		355					360					365			
Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp
	370					375					380				
Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe
385					390					395					400
Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro
				405					410					415	
Asp	Ser	Leu	Pro	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg
			420					425					430		
Gly	Arg	Ile	Leu	His	Asn	Gly	Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu
		435					440					445			
Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	Leu	Gly	Ser	Gly
	450					455					460				
Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val
465					470					475					480
Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr
				485					490					495	
Ala	Asn	Arg	Pro	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His
			500					505					510		

FIG. 13. (CONTINUED)

+

09854356-020400

+

26/47

Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys
		515					520					525			
Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu	Cys
		530				535					540				
Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys
545					550					555					560
Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys
				565					570					575	
Phe	Gly	Pro	Glu	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp
			580					585					590		
Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu
		595					600					605			
Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	Gly	Ala	Cys	Gln
	610					615					620				
Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys
625					630					635					640
Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser	Gln	Asn	Glu
				645					650					655	
Asp	Leu	Gly	Pro	Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr	Arg	Ser	Leu
			660					665					670		
Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	Glu	Glu	Tyr	Leu
		675					680					685			
Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro	Gly	Ala	Gly
	690					695					700				
Gly	Met	Val	His	His	Arg	His	Arg	*	*						
705					710				714						

FIG. 13.(CONTINUED)

+

09051356-020402

204020" 95E45860

27/47

Met	Glu	Leu	Ala	Ala	Trp	Cys	Arg	Trp	Gly	Phe	Leu	Leu	Ala	Leu	Leu		
1				5					10					15			
Pro	Pro	Gly	Ile	Ala	Gly	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys		
			20					25					30				
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His		
			35				40					45					
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr		
	50					55					60						
Val	Pro	Ala	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val		
65					70					75					80		
Gln	Gly	Tyr	Met	Leu	Ile	Ala	His	Asn	Gln	Val	Lys	Arg	Val	Pro	Leu		
				85					90					95			
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Lys	Tyr		
			100					105					110				
Ala	Leu	Ala	Val	Leu	Asp	Asn	Arg	Asp	Pro	Gln	Asp	Asn	Val	Ala	Ala		
		115				120						125					
Ser	Thr	Pro	Gly	Arg	Thr	Pro	Glu	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg		
	130					135					140						
Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Arg	Gly	Asn	Pro		
145					150					155					160		
Gln	Leu	Cys	Tyr	Gln	Asp	Met	Val	Leu	Trp	Lys	Asp	Val	Phe	Arg	Lys		
				165					170					175			
Asn	Asn	Gln	Leu	Ala	Pro	Val	Asp	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala		
			180					185					190				
Cys	Pro	Pro	Cys	Ala	Pro	Ala	Cys	Lys	Asp	Asn	His	Cys	Trp	Gly	Glu		
		195					200					205					
Ser	Pro	Glu	Asp	Cys	Gln	Ile	Leu	Thr	Gly	Thr	Ile	Cys	Thr	Ser	Gly		
	210					215					220						
Cys	Ala	Arg	Cys	Lys	Gly	Arg	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln		
225					230					235					240		
Cys	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys		
				245					250					255			

FIG. 14. (SEQ ID NO: 8)

+

[illegible]

+

+

29/47

Asn	Ser	Leu	Cys	Ala	His	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln
		515					520					525			
Cys	Val	Asn	Cys	Ser	His	Phe	Leu	Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu
	530					535					540				
Cys	Arg	Val	Trp	Lys	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Ser	Asp	Lys	Arg
545					550					555					560
Cys	Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Ser	Ser	Glu	Thr
				565					570					575	
Cys	Phe	Gly	Ser	Glu	Ala	Asp	Gln	Cys	Ala	Ala	Cys	Ala	His	Tyr	Lys
			580					585					590		
Asp	Ser	Ser	Ser	Cys	Val	Ala	Arg	Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp
		595					600					605			
Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	Tyr	Pro	Asp	Glu	Glu	Gly	Ile	Cys
	610					615					620				
Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Glu
625					630					635					640
Arg	Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Val	Thr	Phe		
				645					650				654		

FIG. 14. (CONTINUED)

09854356 . 020402

+

30/47

ATG	GAG	CTG	GCG	GCC	TTG	TGC	CGC	TGG	GGG	CTC	CTC	CTC	GCC	CTC	45
Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	
1				5					10					15	
TTG	CCC	CCC	GGA	GCC	GCG	AGC	ACC	CAA	GTG	TGC	ACC	GGC	ACA	GAC	90
Leu	Pro	Pro	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	
				20					25					30	
ATG	AAG	CTG	CGG	CTC	CCT	GCC	AGT	CCC	GAG	ACC	CAC	CTG	GAC	ATG	135
Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	
				35					40					45	
CTC	CGC	CAC	CTC	TAC	CAG	GGC	TGC	CAG	GTG	GTG	CAG	GGA	AAC	CTG	180
Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	
				50					55					60	
GAA	CTC	ACC	TAC	CTG	CCC	ACC	AAT	GCC	AGC	CTG	TCC	TTC	CTG	CAG	225
Glu	Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	
				65					70					75	
GAT	ATC	CAG	GAG	GTG	CAG	GGC	TAC	GTG	CTC	ATC	GCT	CAC	AAC	CAA	270
Asp	Ile	Gln	Glu	Val	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	
				80					85					90	
GTG	AGG	CAG	GTC	CCA	CTG	CAG	AGG	CTG	CGG	ATT	GTG	CGA	GGC	ACC	315
Val	Arg	Gln	Val	Pro	Leu	Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	
				95					100					105	
CAG	CTC	TTT	GAG	GAC	AAC	TAT	GCC	CTG	GCC	GTG	CTA	GAC	AAT	GGA	360
Gln	Leu	Phe	Glu	Asp	Asn	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	
				110					115					120	
GAC	CCG	CTG	AAC	AAT	ACC	ACC	CCT	GTC	ACA	GGG	GCC	TCC	CCA	GGA	405
Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	
				125					130					135	
GGC	CTG	CGG	GAG	CTG	CAG	CTT	CGA	AGC	CTC	ACA	GAG	ATC	TTG	AAA	450
Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	
				140					145					150	
GGA	GGG	GTC	TTG	ATC	CAG	CGG	AAC	CCC	CAG	CTC	TGC	TAC	CAG	GAC	495
Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	Leu	Cys	Tyr	Gln	Asp	
				155					160					165	
ACG	ATT	TTG	TGG	AAG	GAC	ATC	TTC	CAC	AAG	AAC	AAC	CAG	CTG	GCT	540
Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	Asn	Gln	Leu	Ala	
				170					175					180	

FIG. 15. (SEQ ID NO:9)

31/47

CTC	ACA	CTG	ATA	GAC	ACC	AAC	CGC	TCT	CGG	GCC	TGC	CAC	CCC	TGT	585
Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	His	Pro	Cys	
				185					190					195	
TCT	CCG	ATG	TGT	AAG	GGC	TCC	CGC	TGC	TGG	GGA	GAG	AGT	TCT	GAG	630
Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	Ser	Glu	
				200					205					210	
GAT	TGT	CAG	AGC	CTG	ACG	CGC	ACT	GTC	TGT	GCC	GGT	GGC	TGT	GCC	675
Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys	Ala	
				215					220					225	
CGC	TGC	AAG	GGG	CCA	CTG	CCC	ACT	GAC	TGC	TGC	CAT	GAG	CAG	TGT	720
Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	
				230					235					240	
GCT	GCC	GGC	TGC	ACG	GGC	CCC	AAG	CAC	TCT	GAC	TGC	CTG	GCC	TGC	765
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	
				245					250					255	
CTC	CAC	TTC	AAC	CAC	AGT	GGC	ATC	TGT	GAG	CTG	CAC	TGC	CCA	GCC	810
Leu	His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	
				260					265					270	
CTG	GTC	ACC	TAC	AAC	ACA	GAC	ACG	TTT	GAG	TCC	ATG	CCC	AAT	CCC	855
Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	
				275					280					285	
GAG	GGC	CGG	TAT	ACA	TTC	GGC	GCC	AGC	TGT	GTG	ACT	GCC	TGT	CCC	900
Glu	Glu	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	
				290					295					300	
TAC	AAC	TAC	CTT	TCT	ACG	GAC	GTG	GGA	TCC	TGC	ACC	CTC	GTC	TGC	945
Tyr	Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	
				305					310					315	
CCC	CTG	CAC	AAC	CAA	GAG	GTG	ACA	GCA	GAG	GAT	GGA	ACA	CAG	CGG	990
Pro	Leu	His	Asn	Gln	Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	
				320					325					330	
TGT	GAG	AAG	TGC	AGC	AAG	CCC	TGT	GCC	CGA	GTG	TGC	TAT	GGT	CTG	1035
Cys	Glu	Lys	Cys	Ser	Lys	Pro	Cys	Ala	Arg	Val	Cys	Tyr	Gly	Leu	
				335					340					345	
GGC	ATG	GAG	CAC	TTG	CGA	GAG	GTG	AGG	GCA	GTT	ACC	AGT	GCC	AAT	1080
Gly	Met	Glu	His	Leu	Arg	Glu	Val	Arg	Ala	Val	Thr	Ser	Ala	Asn	
				350					355					360	

FIG. 15. (CONTINUED)

32/47

ATC	CAG	GAG	TTT	GCT	GGC	TGC	AAG	AAG	ATC	TTT	GGG	AGC	CTG	GCA	1125
Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	Lys	Ile	Phe	Gly	Ser	Leu	Ala	
				365					370					375	
TTT	CTG	CCG	GAG	AGC	TTT	GAT	GGG	GAC	CCA	GCC	TCC	AAC	ACT	GCC	1170
Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	
				380					385					390	
CCG	CTC	CAG	CCA	GAG	CAG	CTC	CAA	GTG	TTT	GAG	ACT	CTG	GAA	GAG	1215
Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	Glu	Thr	Leu	Glu	Glu	
				395					400					405	
ATC	ACA	GGT	TAC	CTA	TAC	ATC	TCA	GCA	TGG	CCG	GAC	AGC	CTG	CCT	1260
Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	Pro	
				410					415					420	
GAC	CTC	AGC	GTC	TTC	CAG	AAC	CTG	CAA	GTA	ATC	CGG	GGA	CGA	ATT	1305
Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	Gly	Arg	Ile	
				425					430					435	
CTG	CAC	AAT	GGC	GCC	TAC	TCG	CTG	ACC	CTG	CAA	GGG	CTG	GGC	ATC	1350
Leu	His	Asn	Gly	Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	Gly	Ile	
				440					445					450	
AGC	TGG	CTG	GGG	CTG	CGC	TCA	CTG	AGG	GAA	CTG	GGC	AGT	GGA	CTG	1395
Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	Leu	Gly	Ser	Gly	Leu	
				455					460					465	
GCC	CTC	ATC	CAC	CAT	AAC	ACC	CAC	CTC	TGC	TTC	GTG	CAC	ACG	GTG	1440
Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val	
				470					475					480	
CCC	TGG	GAC	CAG	CTC	TTT	CGG	AAC	CCG	CAC	CAA	GCT	CTG	CTC	CAC	1485
Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	
				485					490					495	
ACT	GCC	AAC	CGG	CCA	GAG	GAC	GAG	TGT	GTG	GGC	GAG	GGC	CTG	GCC	1530
Thr	Ala	Asn	Arg	Pro	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	
				500					505					510	
TGC	CAC	CAG	CTG	TGC	GCC	CGA	GGG	CAC	TGC	TGG	GGT	CCA	GGG	CCC	1575
Cys	His	Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	
				515					520					525	
ACC	CAG	TGT	GTC	AAC	TGC	AGC	CAG	TTC	CTT	CGG	GGC	CAG	GAG	TGC	1620
Thr	Gln	Cys	Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	
				530					535					540	

FIG. 15. (CONTINUED)

33/47

GTG	GAG	GAA	TGC	CGA	GTA	CTG	CAG	GGG	CTC	CCC	AGG	GAG	TAT	GTG	1665
Val	Glu	Glu	Cys	Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	555
				545											
AAT	GCC	AGG	CAC	TGT	TTG	CCG	TGC	CAC	CCT	GAG	TGT	CAG	CCC	CAG	1710
Asn	Ala	Arg	His	Cys	Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	570
				560											
AAT	GGC	TCA	GTG	ACC	TGT	TTT	GGA	CCG	GAG	GCT	GAC	CAG	TGT	GTG	1755
Asn	Gly	Ser	Val	Thr	Cys	Phe	Gly	Pro	Glu	Ala	Asp	Gln	Cys	Val	585
				575											
GCC	TGT	GCC	CAC	TAT	AAG	GAC	CCT	CCC	TTC	TGC	GTG	GCC	CGC	TGC	1800
Ala	Cys	Ala	His	Tyr	Lys	Asp	Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	600
				590											
CCC	AGC	GGT	GTG	AAA	CCT	GAC	CTC	TCC	TAC	ATG	CCC	ATC	TGG	AAG	1845
Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	615
				605											
TTT	CCA	GAT	GAG	GAG	GGC	GCA	TGC	CAG	CCT	TGC	CCC	ATC	AAC	TGC	1890
Phe	Pro	Asp	Glu	Glu	Gly	Ala	Cys	Gln	Pro	Cys	Pro	Ile	Asn	Cys	630
				620											
ACC	CAC	TCC	TGT	GTG	GAC	CTG	GAT	GAC	AAG	GGC	TGC	CCC	GCC	GAG	1935
Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys	Gly	Cys	Pro	Ala	Glu	645
				635											
CAG	AGA	GCC	AGC	CCT	CTG	ACG	TCC	ATC	ATC	TCT	GCG	GTG	GTT	GGC	1980
Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser	Ile	Ile	Ser	Ala	Val	Val	Gly	660
				650											
ATT	CTG	CTG	GTC	GTG	GTC	TTG	GGG	GTG	GTC	TTT	GGG	ATC	CTC	ATC	2025
Ile	Leu	Leu	Val	Val	Val	Leu	Gly	Val	Val	Phe	Gly	Ile	Leu	Ile	675
				665											
AAG	CGA	CGG	CAG	CAG	AAG	ATC	CGG	AAG	TAC	ACG	ATG	CGG	AGA	CTG	2070
Lys	Arg	Arg	Gln	Gln	Lys	Ile	Arg	Lys	Tyr	Thr	Met	Arg	Arg	Leu	690
				680											
CTG	CAG	GAA	ACG	GAG	CTG	GTG	GAG	CCG	CTG	ACA	CCT	AGC	GGA	GCG	2115
Leu	Gln	Glu	Thr	Glu	Leu	Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly	Ala	705
				695											
ATG	CCC	AAC	CAG	GCG	CAG	ATG	CGG	ATC	CTG	AAA	GAG	ACG	GAG	CTG	2160
Met	Pro	Asn	Gln	Ala	Gln	Met	Arg	Ile	Leu	Lys	Glu	Thr	Glu	Leu	720
				710											

FIG. 15. (CONTINUED)

34/47

AGG	AAG	GTG	AAG	GTG	CTT	GGA	TCT	GGC	GCT	TTT	GGC	ACA	GTC	TAC	2205
Arg	Lys	Val	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr	
				725					730					735	
AAG	GGC	ATC	TGG	ATC	CCT	GAT	GGG	GAG	AAT	GTG	AAA	ATT	CCA	GTG	2250
Lys	Gly	Ile	Trp	Ile	Pro	Asp	Gly	Glu	Asn	Val	Lys	Ile	Pro	Val	
				740					745					750	
GCC	ATC	AAA	GTG	TTG	AGG	GAA	AAC	ACA	TCC	CCC	AAA	GCC	AAC	AAA	2295
Ala	Ile	Lys	Val	Leu	Arg	Glu	Asn	Thr	Ser	Pro	Lys	Ala	Asn	Lys	
				755					760					765	
GAA	ATC	TTA	GAC	GAA	GCA	TAC	GTG	ATG	GCT	GGT	GTG	GGC	TCC	CCA	2340
Glu	Ile	Leu	Asp	Glu	Ala	Tyr	Val	Met	Ala	Gly	Val	Gly	Ser	Pro	
				770					775					780	
TAT	GTC	TCC	CGC	CTT	CTG	GGC	ATC	TGC	CTG	ACA	TCC	ACG	GTG	CAG	2385
Tyr	Val	Ser	Arg	Leu	Leu	Gly	Ile	Cys	Leu	Thr	Ser	Thr	Val	Gln	
				785					790					795	
CTG	GTG	ACA	CAG	CTT	ATG	CCC	TAT	GGC	TGC	CTC	TTA	GAC	CAT	GTC	2430
Leu	Val	Thr	Gln	Leu	Met	Pro	Tyr	Gly	Cys	Leu	Leu	Asp	His	Val	
				800					805					810	
CGG	GAA	AAC	CGC	GGA	CGC	CTG	GGC	TCC	CAG	GAC	CTG	CTG	AAC	TGG	2475
Arg	Glu	Asn	Arg	Gly	Arg	Leu	Gly	Ser	Gln	Asp	Leu	Leu	Asn	Trp	
				815					820					825	
TGT	ATG	CAG	ATT	GCC	AAG	GGG	ATG	AGC	TAC	CTG	GAG	GAT	GTG	CGG	2520
Cys	Met	Gln	Ile	Ala	Lys	Gly	Met	Ser	Tyr	Leu	Glu	Asp	Val	Arg	
				830					835					840	
CTC	GTA	CAC	AGG	GAC	TTG	GCC	GCT	CGG	AAC	GTG	CTG	GTC	AAG	AGT	2565
Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Lys	Ser	
				845					850					855	
CCC	AAC	CAT	GTC	AAA	ATT	ACA	GAC	TTC	GGG	CTG	GCT	CGG	CTG	CTG	2610
Pro	Asn	His	Val	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Ala	Arg	Leu	Leu	
				860					865					870	
GAC	ATT	GAC	GAG	ACA	GAG	TAC	CAT	GCA	GAT	GGG	GGC	AAG	GTG	CCC	2655
Asp	Ile	Asp	Glu	Thr	Glu	Tyr	His	Ala	Asp	Gly	Gly	Lys	Val	Pro	
				875					880					885	
ATC	AAG	TGG	ATG	GCG	CTG	GAG	TCC	ATT	CTC	CGC	CGG	CGG	TTC	ACC	2700
Ile	Lys	Trp	Met	Ala	Leu	Glu	Ser	Ile	Leu	Arg	Arg	Arg	Phe	Thr	
				890					895					900	

FIG. 15. (CONTINUED)

35/47

CAC	CAG	AGT	GAT	GTG	TGG	AGT	TAT	GGT	GTG	ACT	GTG	TGG	GAG	CTG	2745
His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Val	Trp	Glu	Leu	
				905					910					915	
ATG	ACT	TTT	GGG	GCC	AAA	CCT	TAC	GAT	GGG	ATC	CCA	GCC	CGG	GAG	2790
Met	Thr	Phe	Gly	Ala	Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Ala	Arg	Glu	
				920					925					930	
ATC	CCT	GAC	CTG	CTG	GAA	AAG	GGG	GAG	CGG	CTG	CCC	CAG	CCC	CCC	2835
Ile	Pro	Asp	Leu	Leu	Glu	Lys	Lgy	Glu	Arg	Leu	Pro	Gln	Pro	Pro	
				935					940					945	
ATC	TGC	ACC	ATT	GAT	GTC	TAC	ATG	ATC	ATG	GTC	AAA	TGT	TGG	ATG	2880
Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Ile	Met	Val	Lys	Cys	Trp	Met	
				950					955					960	
ATT	GAC	TCT	GAA	TGT	CGG	CCA	AGA	TTC	CGG	GAG	TTG	GTG	TCT	GAA	2925
Ile	Asp	Ser	Glu	Cys	Arg	Pro	Arg	Phe	Arg	Glu	Leu	Val	Ser	Glu	
				965					970					975	
TTC	TCC	CGC	ATG	GCC	AGG	GAC	CCC	CAG	CGC	TTT	GTG	GTC	ATC	CAG	2970
Phe	Ser	Arg	Met	Ala	Arg	Asp	Pro	Gln	Arg	Phe	Val	Val	Ile	Gln	
				980					985					990	
AAT	GAG	GAC	TTG	GGC	CCA	GCC	AGT	CCC	TTG	GAC	AGC	ACC	TTC	TAC	3015
Asn	Glu	Asp	Leu	Gly	Pro	Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr	
				995					1000					1005	
CGC	TCA	CTG	CTG	GAG	GAC	GAT	GAC	ATG	GGG	GAC	CTG	GTG	GAT	GCT	3060
Arg	Ser	Leu	Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	
				1010					1015					1020	
GAG	GAG	TAT	CTG	GTA	CCC	CAG	CAG	GGC	TTC	TTC	TGT	CCA	GAC	CCT	3105
Glu	Glu	Tyr	Leu	Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	
				1025					1030					1035	
GCC	CCG	GGC	GCT	GGG	GGC	ATG	GTC	CAC	CAC	AGG	CAC	CGC	AGC	TCA	3150
Ala	Pro	Gly	Ala	Gly	Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	
				1040					1045					1050	
TCT	ACC	AGG	AGT	GGC	GGT	GGG	GAC	CTG	ACA	CTA	GGG	CTG	GAG	CCC	3195
Ser	Thr	Arg	Ser	Gly	Gly	Gly	Asp	Leu	Thr	Leu	Gly	Leu	Glu	Pro	
				1055					1060					1065	
TCT	GAA	GAG	GAG	GCC	CCC	AGG	TCT	CCA	CTG	GCA	CCC	TCC	GAA	GGG	3240
Ser	Glu	Glu	Glu	Ala	Pro	Arg	Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	
				1070					1075					1080	

FIG. 15. (CONTINUED)

+

36/47

GCT	GGC	TCC	GAT	GTA	TTT	GAT	GGT	GAC	CTG	GGA	ATG	GGG	GCA	GCC	3285
Ala	Gly	Ser	Asp	Val	Phe	Asp	Gly	Asp	Leu	Gly	Met	Gly	Ala	Ala	
				1085					1090					1095	
AAG	GGG	CTG	CAA	AGC	CTC	CCC	ACA	CAT	GAC	CCC	AGC	CCT	CTA	CAG	3330
Lys	Gly	Leu	Gln	Ser	Leu	Pro	Thr	His	Asp	Pro	Ser	Pro	Leu	Gln	
				1100					1105					1110	
CGG	TAC	AGT	GAG	GAC	CCC	ACA	GTA	CCC	CTG	CCC	TCT	GAG	ACT	GAT	3375
Arg	Tyr	Ser	Glu	Asp	Pro	Thr	Val	Pro	Leu	Pro	Ser	Glu	Thr	Asp	
				1115					1120					1125	
GGC	TAC	GTT	GCC	CCC	CTG	ACC	TGC	AGC	CCC	CAG	CCT	GAA	TAT	GTG	3420
Gly	Tyr	Val	Ala	Pro	Leu	Thr	Cys	Ser	Pro	Gln	Pro	Glu	Tyr	Val	
				1130					1135					1140	
AAC	CAG	CCA	GAT	GTT	CGG	CCC	CAG	CCC	CCT	TCG	CCC	CGA	GAG	GGC	3465
Asn	Gln	Pro	Asp	Val	Arg	Pro	Gln	Pro	Pro	Ser	Pro	Arg	Glu	Gly	
				1145					1150					1155	
CCT	CTG	CCT	GCT	GCC	CGA	CCT	GCT	GGT	GCC	ACT	CTG	GAA	AGG	CCC	3510
Pro	Leu	Pro	Ala	Ala	Arg	Pro	Ala	Gly	Ala	Thr	Leu	Glu	Arg	Pro	
				1160					1165					1170	
AAG	ACT	CTC	TCC	CCA	GGG	AAG	AAT	GGG	GTC	GTC	AAA	GAC	GTT	TTT	3555
Lys	Thr	Leu	Ser	Pro	Gly	Lys	Asn	Gly	Val	Val	Lys	Asp	Val	Phe	
				1175					1180					1185	
GCC	TTT	GGG	GGT	GCC	GTG	GAG	AAC	CCC	GAG	TAC	TTG	ACA	CCC	CAG	3600
Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu	Tyr	Leu	Thr	Pro	Gln	
				1190					1195					1200	
GGA	GGA	GCT	GCC	CCT	CAG	CCC	CAC	CCT	CCT	CCT	GCC	TTC	AGC	CCA	3645
Gly	Gly	Ala	Ala	Pro	Gln	Pro	His	Pro	Pro	Pro	Ala	Phe	Ser	Pro	
				1205					1210					1215	
GCC	TTC	GAC	AAC	CTC	TAT	TAC	TGG	GAC	CAG	GAC	CCA	CCA	GAG	CGG	3690
Ala	Phe	Asp	Asn	Leu	Tyr	Tyr	Trp	Asp	Gln	Asp	Pro	Pro	Glu	Arg	
				1220					1225					1230	
GGG	GCT	CCA	CCC	AGC	ACC	TTC	AAA	GGG	ACA	CCT	ACG	GCA	GAG	AAC	3735
Gly	Ala	Pro	Pro	Ser	Thr	Phe	Lys	Gly	Thr	Pro	Thr	Ala	Glu	Asn	
				1235					1240					1245	
CCA	GAG	TAC	CTG	GGT	CTG	GAC	GTG	CCA	GTG	TGA					3768
Pro	Glu	Tyr	Leu	Gly	Leu	Asp	Val	Pro	Val						
				1250					1255						

FIG. 15. (CONTINUED)

+

09854356 020402

37/47

ccgggcccga	gccgcaatga	tcatcatgga	gctggcggcc	tggtgccgct	50
gggggttcct	cctcgccctc	ctgccccccg	gaatcgcggg	cacccaagtg	100
tgtaccggca	cagacatgaa	gttgcggtct	cctgccagtc	ctgagaccca	150
cctggacatg	ctccgccacc	tgtaccaggg	ctgtcaggta	gtgcagggca	200
acttggaagt	tacctacgtg	cctgccaatg	ccagcctctc	attcctgcag	250
gacatccagg	aagttcaggg	ttacatgctc	atcgctcaca	accaggtgaa	300
gcgcgtccca	ctgcaaaggc	tgcgcatact	gagagggacc	cagctctttg	350
aggacaagta	tgccctggct	gtgctagaca	accgagatcc	tcaggacaat	400
gtcgccgcct	ccaccccagg	cagaacccca	gaggggctgc	gggagctgca	450
gcttcgaagt	ctcacagaga	tcttgaaggg	aggagttttg	atccgtggga	500
accctcagct	ctgctaccag	gacatggttt	tgtggaagga	cgtcttccgc	550
aagaataacc	aactggctcc	tgtcgatata	gacaccaatc	gttcccgggc	600
ctgtccacct	tgtgcccccg	cctgcaaaga	caatcactgt	tggggtgaga	650
gtccggaaga	ctgtcagatc	ttgactggca	ccatctgtac	cagtggttgt	700
gcccgggtgca	agggccggct	gcccactgac	tgctgccatg	agcagtgtgc	750
cgcaggctgc	acgggccccca	agcattctga	ctgcctggcc	tgccctccact	800
tcaatcatag	tggtatctgt	gagctgcact	gcccagccct	cgtcacctac	850
aacacagaca	cctttgagtc	catgcacaa	cctgagggtc	gctacacctt	900
tggtgccagc	tgcgtgacca	cctgccccta	caactacctg	tctacggaag	950
tgggatcctg	cactctggtg	tgtccccoga	ataaccaaga	ggtcacagct	1000
gaggacggaa	cacagcggtg	tgagaaatgc	agcaagccct	gtgctcgagt	1050
gtgctatggt	ctgggcatgg	agcaccttcg	aggggcgagg	gccatcacca	1100
gtgacaatgt	ccaggagttt	gatggctgca	agaagatctt	tgggagcctg	1150
gcatttttgc	cggagagctt	tgatggggac	ccctcctccg	gcattgctcc	1200
gctgaggcct	gagcagctcc	aagtgttcga	aaccctggag	gagatcacag	1250
gttacctgta	catctcagca	tggccagaca	gtctccgtga	cctcagtgtc	1300
ttccagaacc	ttcgaatcat	tgggggacgg	attctccacg	atggcgcgta	1350
ctcattgaca	ctgcaaggcc	tggggatcca	ctcgctgggg	ctgcgctcac	1400
tgcgggagct	gggcagtgga	ttggctctga	ttcacccgaa	cgcccatctc	1450
tgctttgtac	acactgtacc	ttgggaccag	ctcttccgga	accacatca	1500
ggccctgctc	cacagtggga	accggccgga	agaggacttg	tgcgtctcga	1550
gcggcttggt	ctgtaactca	ctgtgtgccc	acgggcactg	ctggggggcca	1600
gggcccaccc	agtgtgtcaa	ctgcagtcac	ttccttccgg	gccaggagtg	1650
tgtggaggag	tgccgagtat	ggaaggggct	cccccgggag	tatgtgagtg	1700
acaagcgtg	tctgccgtgt	caccccaggt	gtcagcctca	aaacagctca	1750
gagacctgct	ttggatcgga	ggctgatcag	tgtgcagcct	gcgcccacta	1800
caaggactcg	tcctcctgtg	tggctcgctg	ccccagtggt	gtgaaaccgg	1850
acctctccta	catgcccata	tggaaagtacc	cggatgagga	gggcatatgc	1900
cagccgtgcc	ccatcaactg	cacccactcc	tgtgtggatc	tggatgaacg	1950
aggctgccc	gcagagcaga	gagccagccc	ggtgacattc	atcattgcaa	2000
ctgtagaggg	cgtcctgctg	ttcctgatct	tagtggtggt	cgtttgaatc	2050
ctaatacaac	gaaggagaca	gaagatccgg	aagtatacga	tgcgtaggct	2100
gctgcaggaa	actgagttag	tggagccgct	gacgcccagc	ggagcaatgc	2150
ccaaccaggc	tcagatgcgg	atcctaaaag	agacggagct	aaggaagggtg	2200
aagggtgctt	gatcaggagc	ttttggcact	gtctacaagg	gcattctggat	2250
cccagatggg	gagaatgtga	aaatccccgt	ggctatcaag	gtgttgagag	2300
aaaacacatc	tcctaaagcc	aacaaagaaa	ttctagatga	agcgtatgtg	2350

FIG. 16. (SEQ ID NO: 10)

38/47

atggctggtg	tgggttctcc	gtatgtgtcc	cgcctcctgg	gcctctgcct	2400
gacatccaca	gtacagctgg	tgacacagct	tatgccctac	ggctgccttc	2450
tggaccatgt	ccgagaacac	cgaggtcgcc	taggctccca	ggacctgctc	2500
aactggtgtg	ttcagattgc	caaggggatg	agctacctgg	aggacgtgcg	2550
gcttgtacac	agggacctgg	ctgcccggaa	tgtgctagtc	aagagtccca	2600
accacgtcaa	gattacagat	ttcgggctgg	ctcggctgct	ggacattgat	2650
gagacagagt	accatgcaga	tgggggcaag	gtgcccata	aatggatggc	2700
atttgaatct	attctcagac	gccggttcac	ccatcagagt	gatgtgtgga	2750
gctatggagt	gactgtgtgg	gagctgatga	cttttggggc	caaaccttac	2800
gatggaatcc	cagcccggga	gatccctgat	ttgctggaga	agggagaacg	2850
cctacctcag	cctccaatct	gcaccattga	tgtctacatg	attatggtca	2900
aatgttggat	gattgactct	gaatgtcgcc	cgagattccg	ggagttggtg	2950
tcagaatttt	cacgtatggc	gagggacccc	cagcgttttg	tggatcatcca	3000
gaacgaggac	ttgggcccac	ccagccccc	ggacagtacc	ttctaccgtt	3050
cactgctgga	agatgatgac	atgggtgacc	tggtagacgc	tgaagagtat	3100
ctggtgcccc	agcagggatt	cttctccccg	gaccctaccc	caggcactgg	3150
gagcacagcc	catagaaggc	accgcagctc	gtccaccagg	agtggaggtg	3200
gtgagctgac	actgggcctg	gagccctcgg	aagaagggcc	ccccagatct	3250
ccactggctc	cctcgggaag	ggctggctcc	gatgtgtttg	atggtgacct	3300
ggcaatgggg	gtaaccaaag	ggctgcagag	cctctctcca	catgacctca	3350
gccctctaca	gcggtacagc	gaggacccca	cattacctct	gccccccgag	3400
actgatggct	atgttgctcc	cctggcctgc	agccccccagc	ccgagtatgt	3450
gaaccaatca	gaggttcagc	ctcagcctcc	tttaacccca	gagggtcctc	3500
tgcctcctgt	ccggcctgct	ggtgctactc	tagaaagacc	caagactctc	3550
tctcctggga	agaatggggg	tgtcaaagac	gtttttgcct	tcggggggtgc	3600
tgtggagaac	cctgaatact	tagtaccgag	agaaggcact	gcctctccgc	3650
cccacccttc	tcctgccttc	agcccagcct	ttgacaacct	ctattactgg	3700
gaccagaact	catcggagca	ggggcctcca	ccaagtaact	ttgaagggac	3750
ccccactgca	gagaaccctg	agtacctagg	cctggatgta	cctgtatgag	3800
acgtgtgcag	acgtcctgtg	ctttcagagt	ggggaaggcc	tgacttgtgg	3850
tctccatcgc	cacaaagcag	ggagagggtc	ctctggccac	attacatcca	3900
gggcagacgg	ctctaccagg	aacctgcccc	gaggaacctt	tccttgctgc	3850
ttgaa	3955				

FIG. 16. (CONTINUED)

Herceptin Binding by Direct Elisa 10/5/99

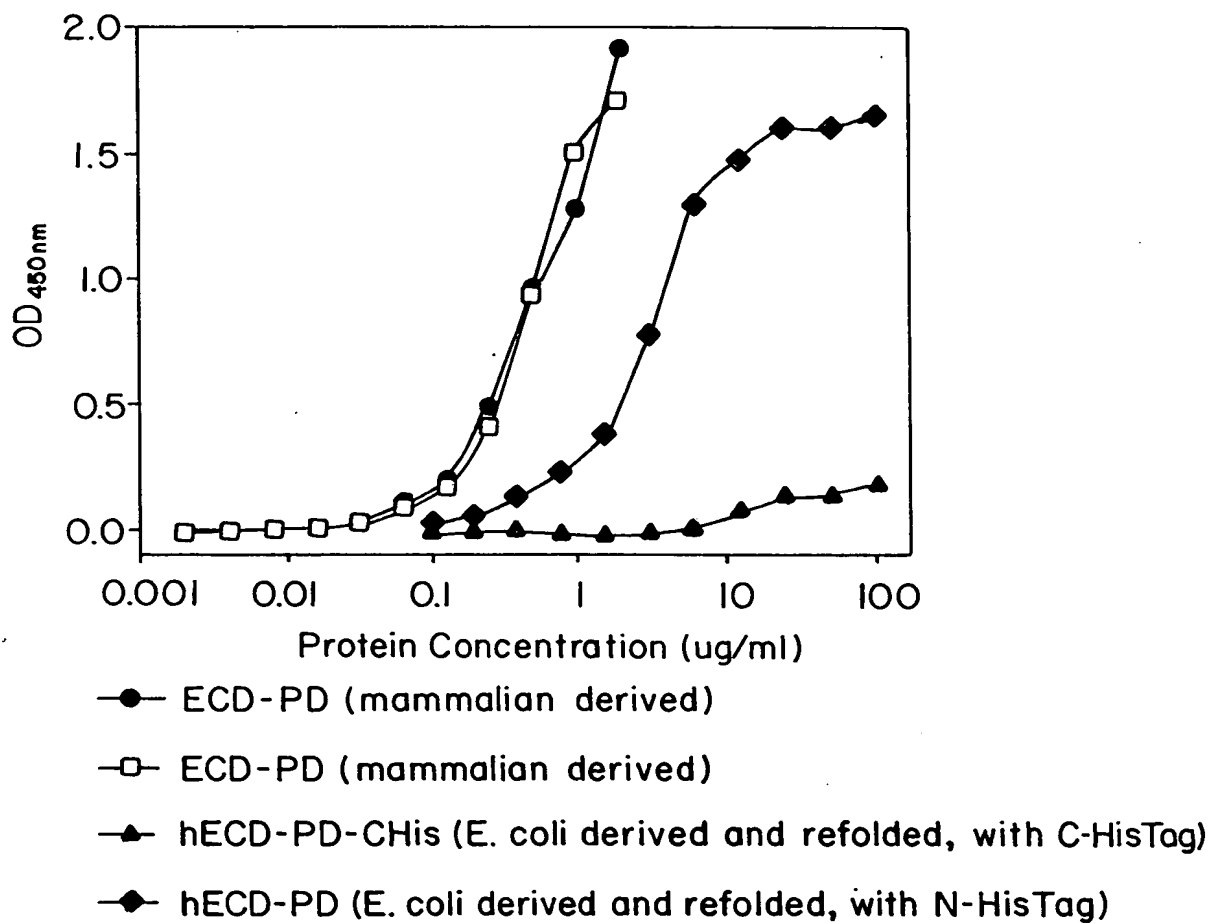
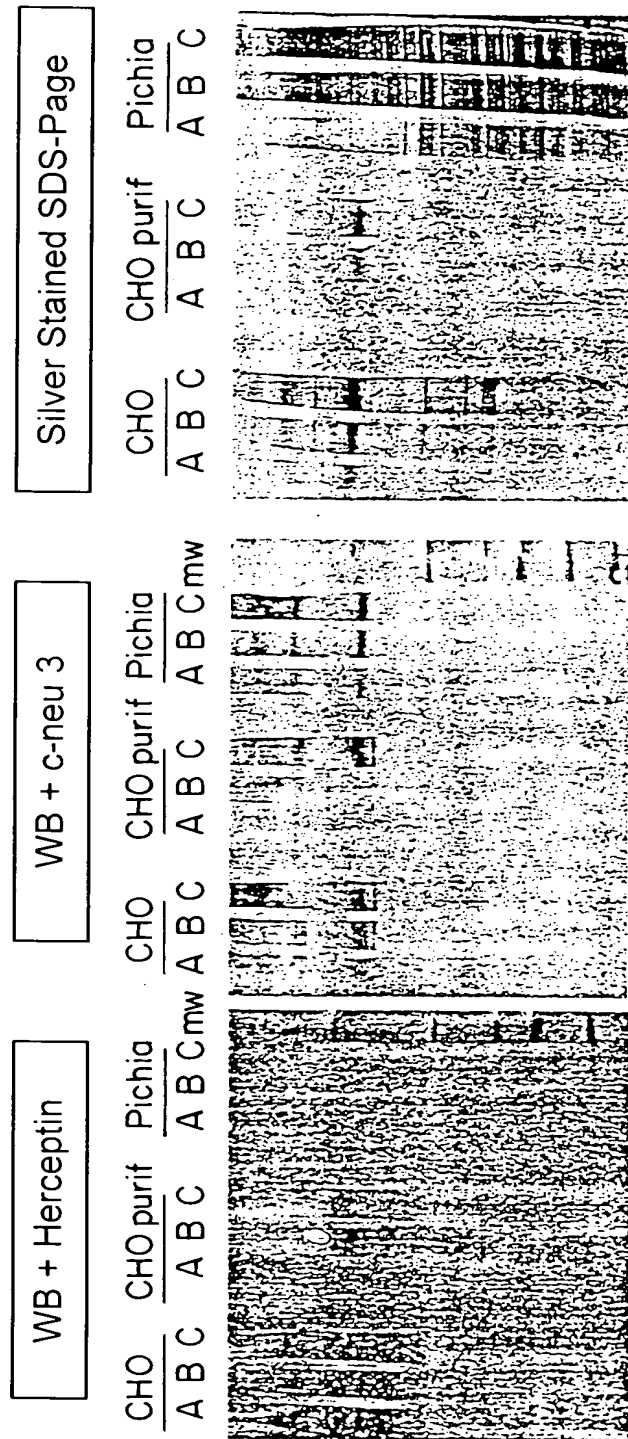


FIG. 17.

Comparison of Her2neu ECD-PD Expression in CHO-K1 (S/SF) and Pichia (Non reducing conditions)



Legend: CHO; A, B, C = 2,5µl/ 5µl/ 10µl
CHO purif; A, B, C = 125ng/ 250ng/ 500ng
Pichia; A, B, C = 2,5µl/ 5µl/ 10µl from a 1/30 dilution of OD 120

FIG. 18.

41/47

atggagctgg	cggcctggtg	ccgttggggg	ttcctcctcg	ccctcctgtc	50
ccccggagcc	gcggttaccc	aagtgtgtac	cgttaccgac	atgaagttgc	100
gactccctgc	cagtcctgag	acccacctgg	acatgcttcg	ccacctctac	150
cagggctgtc	aggtggtgca	gggcaatttg	gagcttacct	acctgcccgc	200
caatgccagc	ctctcattcc	tgcaggacat	ccaggaagtc	cagggataca	250
tgctcatcgc	tcacaaccga	gtgaaacacg	tcccactgca	gaggttgctc	300
atcgtgagag	ggactcagct	ctttgaggac	aagtatgccc	tggctgtgct	350
agacaaccga	gaccctttgg	acaacgtcac	caccgcccgc	ccaggcagaa	400
ccccagaagg	gctgcgggag	ctgcagcttc	gaagtctcac	agagatcttg	450
aagggaggag	ttttgatccg	tgggaaccct	cagctctgct	accaggacat	500
ggttttgtgg	aaggatgtcc	tccgtaagaa	taaccagctg	gtcctgtctg	550
acatggacac	caatcgttcc	cgggcctgtc	caccttgtgc	cccaacctgc	600
aaagacaatc	actgttgggg	tgagagtcct	gaagactgtc	agatcttgac	650
tggcaccatc	tgtactagtg	gctgtgcccg	gtgcaagggc	cggctgcccga	700
ctgactgttg	ccatgagcag	tgtgctgcag	gctgcacggg	tccaagcat	750
tctgactgcc	tggcctgcct	ccacttcaat	catagtggta	tctgtgagct	800
gactgcccgc	gccctcatca	cctacaacac	agacaccttc	gagtccatgc	850
tcaaccctga	gggtcgctac	acctttgggtg	ccagctgtgt	gaccacctgc	900
ccctacaact	acctctccac	ggaagtggga	tcctgcactc	tggctctgtcc	950
cccgaacaac	caagaggtca	cagctgagga	cggaaacacag	cgggtgtgaga	1000
aatgcagcaa	gccctgtgct	ggagtatgct	atggtctggg	catggagcac	1050
ctccgagggg	cgagggccat	caccagtgc	aatatccagg	agtttgctgg	1100
ctgcaagaag	atctttggga	gcctggcatt	tttgccggag	agctttgatg	1150
ggaacccctc	ctccggcggt	gccccactga	agccagagca	tctccaagtg	1200
ttcgaaaccc	tggaggagat	cacaggttac	ctatacattt	cagcatggcc	1250
agagagcttc	caagacctca	gtgtcttcca	gaaccttcgg	gtcattcggg	1300
gacggattct	ccatgatggt	gcttactcat	tgacgttgca	aggcctgggg	1350
attcactcac	tggggctacg	ctcactgcgg	gagctgggca	gtggattggc	1400
tctcattcac	cgcaacaccc	atctctgctt	tgtaaacact	gtaccttggg	1450
accagctctt	ccggaacccg	caccaggccc	tactccacag	tgggaaccgg	1500
ccagaagagg	catgtggtct	tgagggcttg	gtctgtaact	cactgtgtgc	1550
ccgtgggcac	tgctgggggc	cagggcccac	ccagtgtgtc	aactgcagtc	1600
agttcctccg	gggccaggag	tgtgtggagg	agtgccgagt	atggaagggg	1650
ctccccaggg	agtatgtgag	gggcaagcac	tgtctgccat	gccaccccca	1700
gtgtcagcct	caaaacagct	cggagacctg	ctatggatcg	gaggctgacc	1750
agtgtgaggc	ttgtgcccac	tacaaggact	catcttcctg	tgtggctcgc	1800
tgccccagtg	gtgtgaagcc	agacctctcc	tacatgccta	tctggaagta	1850
cccgatgag	gagggcatat	gtcagccatg	cccatcaac	tgcacccact	1900
catgtgtgga	cctggacgaa	cgaggctgcc	cagcagagca	gagagccagc	1950
ccagtgcac	tcatcattgc	aactgtgggtg	ggcgtcctgt	tgttcctgat	2000
catagtgggtg	gtcattggaa	tcctaataca	acgaaggcga	cagaagatcc	2050
ggaagtatac	catgcgtagg	ctgctgcagg	agaccgagct	ggtggagccg	2100
ctgacgcccga	gtggagctgt	gcccacccag	gctcagatgc	ggatcctaaa	2150
ggagacagag	ctaaggaagc	tgaagggtgct	tgggtcagga	gccttcggca	2200
ctgtctacaa	gggcattctgg	atcccagatg	gggagaacgt	gaaaatcccc	2250
gtggccatca	aggtgttgag	ggaaaacaca	tctcctaaag	ctaacaaaga	2300
aatcctagat	gaagcgtacg	tcatggctgg	tgtgggttct	ccatatgtgt	2350

FIG. 19. (SEQ ID NO: 11)

42/47

cccgccctcct	gggcatctgc	ctgacatcca	cagtgcagct	ggtgacacag	2400
cttatgccct	atggctgcct	tctggaccat	gtccgagAAC	accgaggtcg	2450
cttaggctcc	caggacctgc	tcaactgggtg	tgttcagatt	gccaagggga	2500
tgagctacct	ggaggaagtt	cggcttggtc	acagggacct	agctgcccga	2550
aacgtgctag	tcaagagtcc	caaccacgtc	aagattaccg	acttcgggct	2600
ggcacggctg	ctggacattg	atgagactga	ataccatgca	gatgggggca	2650
aggtgccccat	caagtggatg	gcattggaat	ctattctcag	acgccgggttc	2700
actcatcaga	gtgatgtgtg	gagctatggt	gtgactgtgt	gggagctgat	2750
gacctttggg	gccaaacctt	acgatgggat	cccagctcgg	gagatccctg	2800
at ttgctgga	gaagggagaa	cgcctacctc	agcctccaat	ctgcaccatc	2850
gacgtctaca	tgatcatggt	caa atgttggt	atgattgact	ccgaatgtcg	2900
cccgagattc	cgggagttgg	tatcagaatt	ctcccgtatg	gcaagggacc	2950
cccagcgctt	tgtggtcatc	cagaacgagg	acttagggcc	ctccagcccc	3000
atggacagca	ccttctaccg	ttcactgctg	gaggatgatg	acatggggga	3050
gctgggtcgat	gctgaagagt	acctggtacc	ccagcaggga	ttctttctccc	3100
cagaccctgc	cctaggtact	gggagcacag	cccaccgcag	acaccgcagc	3150
tcgtcggcca	ggagtggcgg	tggtgagctg	acactgggcc	tggagccctc	3200
ggaagaagag	ccccccagat	ctccactggc	tccctccgaa	ggggctggct	3250
ccgatgtgtt	tgatgggtgac	ctggcagtggt	gggtaaccaa	aggactgcag	3300
agcctctctc	cacatgacct	cagccctcta	cagcgggtaca	gtgaggatcc	3350
cacattacct	ctgccccccg	agactgatgg	ctacgttgct	cccctggcct	3400
gcagccccca	gcccagagtat	gtgaaccagc	cagaggttcg	gcctcagtct	3450
cccttgaccc	cagaggggtcc	tccgcctccc	atccgacctg	ctgggtgctac	3500
tctagaaaga	cccaagactc	tctctcctgg	gaaaaatggg	gttgtcaaag	3550
acgtttttgc	ctttgggggt	gctgtggaga	accctgaata	cctagcacc	3600
agagcaggca	ctgcctctca	gccccaccct	tctcctgcct	tcagcccagc	3650
ctttgacaac	ctctattact	gggaccagaa	ctcatcggag	cagggtcctc	3700
caccaagtac	ctttgaagggt	acccccactg	cagagaaccc	tgagtaccta	3750
ggcctggatg	tgccagtatg	a			3771

FIG. 19.(CONTINUED)

+

43/47

Met	Glu	Leu	Ala	Ala	Trp	Cys	Arg	Trp	Gly	Phe	Leu	Leu	Ala	Leu	Leu		
1				5					10					15			
Ser	Pro	Gly	Ala	Ala	Gly	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys		
			20					25					30				
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His		
		35					40					45					
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr		
	50					55					60						
Leu	Pro	Ala	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val		
65					70					75					80		
Gln	Gly	Tyr	Met	Leu	Ile	Ala	His	Asn	Arg	Val	Lys	His	Val	Pro	Leu		
				85					90					95			
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Lys	Tyr		
			100					105					110				
Ala	Leu	Ala	Val	Leu	Asp	Asn	Arg	Asp	Pro	Leu	Asp	Asn	Val	Thr	Thr		
		115					120					125					
Ala	Ala	Pro	Gly	Arg	Thr	Pro	Glu	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg		
		130					135				140						
Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Arg	Gly	Asn	Pro		
145					150					155					160		
Gln	Leu	Cys	Tyr	Gln	Asp	Met	Val	Leu	Trp	Lys	Asp	Val	Leu	Arg	Lys		
				165					170					175			
Asn	Asn	Gln	Leu	Ala	Pro	Val	Asp	Met	Asp	Thr	Asn	Arg	Ser	Arg	Ala		
			180					185					190				
Cys	Pro	Pro	Cys	Ala	Pro	Thr	Cys	Lys	Asp	Asn	His	Cys	Trp	Gly	Glu		
		195					200					205					
Ser	Pro	Glu	Asp	Cys	Gln	Ile	Leu	Thr	Gly	Thr	Ile	Cys	Thr	Ser	Gly		
		210				215					220						
Cys	Ala	Arg	Cys	Lys	Gly	Arg	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln		
225					230					235					240		
Cys	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys		
				245					250					255			

FIG. 20. (SEQ ID NO: 14)

+

09854356-020402

+

[illegible]

+

098456-02402

+

+

46/47

Leu	Asp	Glu	Ala	Tyr	Val	Met	Ala	Gly	Val	Gly	Ser	Pro	Tyr	Val	Ser	
770						775					780					
Arg	Leu	Leu	Gly	Ile	Cys	Leu	Thr	Ser	Thr	Val	Gln	Leu	Val	Thr	Gln	
785					790					795					800	
Leu	Met	Pro	Tyr	Gly	Cys	Leu	Leu	Asp	His	Val	Arg	Glu	His	Arg	Gly	
				805					810					815		
Arg	Leu	Gly	Ser	Gln	Asp	Leu	Leu	Asn	Trp	Cys	Val	Gln	Ile	Ala	Lys	
			820					825					830			
Gly	Met	Ser	Tyr	Leu	Glu	Glu	Val	Arg	Leu	Val	His	Arg	Asp	Leu	Ala	
		835					840					845				
Ala	Arg	Asn	Val	Leu	Val	Lys	Ser	Pro	Asn	His	Val	Lys	Ile	Thr	Asp	
		850				855					860					
Phe	Gly	Leu	Ala	Arg	Leu	Leu	Asp	Ile	Asp	Glu	Thr	Glu	Tyr	His	Ala	
865					870					875					880	
Asp	Gly	Gly	Lys	Val	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Ser	Ile	Leu	
			885						890					895		
Arg	Arg	Arg	Phe	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	
			900					905					910			
Val	Trp	Glu	Leu	Met	Thr	Phe	Gly	Ala	Lys	Pro	Tyr	Asp	Gly	Ile	Pro	
		915					920					925				
Ala	Arg	Glu	Ile	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu	Arg	Leu	Pro	Gln	
		930				935					940					
Pro	Pro	Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Ile	Met	Val	Lys	Cys	Trp	
945					950					955					960	
Met	Ile	Asp	Ser	Glu	Cys	Arg	Pro	Arg	Phe	Arg	Glu	Leu	Val	Ser	Glu	
				965					970					975		
Phe	Ser	Arg	Met	Ala	Arg	Asp	Pro	Gln	Arg	Phe	Val	Val	Ile	Gln	Asn	
			980					985					990			
Glu	Asp	Leu	Gly	Pro	Ser	Ser	Pro	Met	Asp	Ser	Thr	Phe	Tyr	Arg	Ser	
		995					1000					1005				
Leu	Leu	Glu	Asp	Asp	Asp	Met	Gly	Glu	Leu	Val	Asp	Ala	Glu	Glu	Tyr	
1010						1015					1020					

FIG. 20. (CONTINUED)

+

204020" 9545860

+

47/47

Leu Val Pro Gln Gln Gly Phe Phe Ser Pro Asp Pro Ala Leu Gly Thr
 1025 1030 1035 1040
 Gly Ser Thr Ala His Arg Arg His Arg Ser Ser Ser Ala Arg Ser Gly
 1045 1050 1055
 Gly Gly Glu Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Pro Pro
 1060 1065 1070
 Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp
 1075 1080 1085
 Gly Asp Leu Ala Val Gly Val Thr Lys Gly Leu Gln Ser Leu Ser Pro
 1090 1095 1100
 His Asp Leu Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Leu Pro
 1105 1110 1115 1120
 Leu Pro Pro Glu Thr Asp Gly Tyr Val Ala Pro Leu Ala Cys Ser Pro
 1125 1130 1135
 Gln Pro Glu Tyr Val Asn Gln Pro Glu Val Arg Pro Gln Ser Pro Leu
 1140 1145 1150
 Thr Pro Glu Gly Pro Pro Pro Pro Ile Arg Pro Ala Gly Ala Thr Leu
 1155 1160 1165
 Glu Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp
 1170 1175 1180
 Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Ala Pro
 1185 1190 1195 1200
 Arg Ala Gly Thr Ala Ser Gln Pro His Pro Ser Pro Ala Phe Ser Pro
 1205 1210 1215
 Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asn Ser Ser Glu Gln Gly
 1220 1225 1230
 Pro Pro Pro Ser Thr Phe Glu Gly Thr Pro Thr Ala Glu Asn Pro Glu
 1235 1240 1245
 Tyr Leu Gly Leu Asp Val Pro Val
 1250 1255

FIG. 20. (CONTINUED)

+

2040402-054356